GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 17:35:39 ; Search time 3098 Seconds
                                          (without alignments)
                                          10605.897 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*

Also searched SEQ ID NO:2 (the encoded amino acid seq) in DNA databases

→ same hits found

```
        28:  em_un:*
        29:  em_vi:*
        30:  em_htg_hum:*
        31:  em_htg_inv:*
        32:  em_htg_other:*
        33:  em_htg_mus:*
        34:  em_htg_pln:*
        35:  em_htg_rod:*
        36:  em_htg_mam:*
        37:  em_htg_vrt:*
        38:  em_sy:*
        39:  em_htgo_hum:*
        40:  em_htgo_mus:*
        41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID		Description
	1	1129	100.0	328050	1	AP005275	*Nakagawa*	AP005275 Corynebac
	2	1129	100.0	349980	6	AX127144	*EP 1108790*	AX127144 Sequence
	3	1129	100.0	349980	6	AX127145	"	AX127145 Sequence
	4	564	50.0	564	6	AX120753		AX120753 Sequence
	5	263	23.3	1026	6	AX120754		AX120754 Sequence
	6	133.4	11.8	874	6	AR199611		AR199611 Sequence
c	7	133.4	11.8	14240	1	AE007157		AE007157 Mycobacte
c	8	133.4	11.8	33818	1	MTCY78		Z77165 Mycobacteri
	9	83.2	7.4	31624	1	SCD63		AL161755 Streptomy
	10	80.2	7.1	4692	1	SCAJ10601		AJ010601 Streptomy
c	11	62.4	5.5	42325	1	U00015		U00015 Mycobacteri
	12	62.4	5.5	344050	1	MLEPRTN2		AL583918 Mycobacte
c	13	43	3.8	125020	9	AF429315		AF429315 Homo sapi
	14	42.8	3.8	125020	9	AF429315		AF429315 Homo sapi
	15	42	3.7	199863	2	AC124172		AC124172 Mus muscu
	16	41.8	3.7	176547	2	AC126433		AC126433 Mus muscu
	17	41.8	3.7	236404	2	AC117241		AC117241 Mus muscu
	18	39.4	3.5	36144	1	SC9C5		AL357523 Streptomy
	19	39.4	3.5	38640	1	SCL2		AL137778 Streptomy
	20	38.8	3.4	5610	6	AX278007		AX278007 Sequence
	21	38.8	3.4	5610	6	AX280000		AX280000 Sequence
	22	38.8	3.4	5610	6	AX281189		AX281189 Sequence
	23	38.8	3.4	5610	6	AX323704		AX323704 Sequence
	24	38.8	3.4	5610	6	AX356456		AX356456 Sequence
	25	38.4	3.4	193047	9	CNS0000Q		AL049874 Human chr
	26	38	3.4	2070	1	SCO010584		AJ010584 Streptomy
	27	38	3.4	38084	1	SCE68		AL079345 Streptomy
c	28	38	3.4	179138	9	CNS07EGV		AL606834 Human chr
	29	37.8	3.3	18011	6	AX344937		AX344937 Sequence
	30	37.4	3.3	172746	2	AC025279		AC025279 Homo sapi
c	31	37.4	3.3	174010	2	AC023814		AC023814 Homo sapi
	32	37.4	3.3	177130	3	AC092219		AC092219 Drosophil
c	33	37.4	3.3	179529	2	AC020004		AC020004 Drosophil

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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 16:24:33 ; Search time 325 Seconds
                                           (without alignments)
                                           7823.096 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_101002:*
                 1:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
                 2:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
                 3:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
                 4:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
                 5:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1984.DAT:*
                 6:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
                 7:   /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1986.DAT:*
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                 15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
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                 20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
                 21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
                 22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
                 23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
                 24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	1129	100.0	349980	22	AAH68525	*EP1108790*	C glutamicum codin
2	1129	100.0	349980	22	AAH68526	" "	C glutamicum codin
3	1125.8	99.7	1129	24	ABA96000	*-Appl's DE doc*	Corynebacterium gl
4	564	50.0	564	22	AAH65634		C glutamicum codin
5	263	23.3	1026	22	AAH65635		C glutamicum codin
6	133.4	11.8	1105	19	AAV44589		Mycobacterium tube
c 7	133.4	11.8	4403765	22	AAI99683		Mycobacterium tube
c 8	133.4	11.8	4411529	22	AAI99682		Mycobacterium tube
9	38.8	3.4	5610	22	AAS45462		Chemically pretrea
10	38.8	3.4	5610	24	ABL92281		Chemically treated
11	38.8	3.4	5610	24	ABL49354		Human polynucleoti
12	38.8	3.4	5610	24	AAD22332		Chemically treated
13	38.8	3.4	5610	24	ABK28318		DNA transcription
14	37.8	3.3	18011	24	ABL32035		Human immune syste
15	37.4	3.3	2322	23	ABL28721		Drosophila melanog
c 16	37.4	3.3	4471	23	ABL28720		Drosophila melanog
17	37.2	3.3	950	22	AAK84920		Human immune/haema
18	37.2	3.3	4397	22	AAK84921		Human immune/haema
19	35.4	3.1	1110	21	AAC45795		Arabidopsis thalia
20	35.4	3.1	1380	21	AAC37623		Arabidopsis thalia
21	35.4	3.1	1429	19	AAV04237		Arabidopsis C-14 s
c 22	35	3.1	4639	24	ABK83705		Human cDNA differe
c 23	35	3.1	5924	22	AAI59245		Human polynucleoti
c 24	35	3.1	5925	22	AAI61031		Human polynucleoti
25	34.6	3.1	8996	22	AAS45504		Chemically pretrea
26	34.6	3.1	8996	24	ABK28436		DNA transcription
c 27	34.4	3.0	1401	19	AAV34002		S. peucetius dnrX
c 28	34.4	3.0	2828	21	AAA93121		Human secreted pro
c 29	34.2	3.0	1590	22	AAI71949		Thermus caldophilu
30	34	3.0	566	24	ABQ60238		Human colon cancer
31	33.8	3.0	1420	21	AAZ90582		Maize SINA ortholo
32	33.8	3.0	1428	21	AAC43673		Zea mays DNA fragm
33	33.8	3.0	14649	22	AAS45415		Chemically pretrea
34	33.8	3.0	14649	24	ABK28268		DNA transcription
35	33.6	3.0	89328	24	ABL61995		Colon adenocarcino
c 36	33.4	3.0	365	22	AAK17670		Human brain expres
c 37	33.4	3.0	365	22	AAI24269		Probe #14202 for g
c 38	33.4	3.0	852	21	AAC55802		S. lavendulae MitM
39	33.4	3.0	935	21	AAC00969		Human secreted pro
c 40	33.4	3.0	5581	19	AAV17098		Human pancreatic c
41	33.4	3.0	53500	21	AAC55842		Complete nucleotid
42	33.2	2.9	501	24	ABQ42772		Oligonucleotide fo
c 43	33.2	2.9	501	24	ABQ42773		Oligonucleotide fo
44	33.2	2.9	10713	24	ABL32741		Human immune syste
45	33	2.9	700	22	AAH92867		Human inflammatory

ALIGNMENTS

RESULT 1

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 19:37:19 ; Search time 303 Seconds
                                           (without alignments)
                                           7686.891 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
                 11: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq2:*
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                 13: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
                 14: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
                 15: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
                 16: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
                 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   1129   100.0   1129 11   US-09-941-945A-1   Sequence 1, Appli

	2	1129	100.0	3309400	11	US-09-738-626-1	Sequence 1, Appli
	3	564	50.0	564	11	US-09-738-626-669	Sequence 669, App
	4	263	23.3	1026	11	US-09-738-626-670	Sequence 670, App
	5	84	7.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
	6	81.6	7.2	573	15	US-10-156-761-4983	Sequence 4983, Ap
	7	38.8	3.4	5610	15	US-10-239-676-170	Sequence 170, App
	8	38.4	3.4	2320	15	US-10-027-632-264352	Sequence 264352,
	9	36.4	3.2	671	15	US-10-184-644-346	Sequence 346, App
	10	36.4	3.2	671	15	US-10-184-634-346	Sequence 346, App
c	11	35.6	3.2	453	11	US-09-938-842A-3437	Sequence 3437, Ap
	12	35.4	3.1	1429	8	US-08-879-337-1	Sequence 1, Appli
	13	35	3.1	716	14	US-10-146-731-96	Sequence 96, Appl
	14	35	3.1	716	15	US-10-123-155-96	Sequence 96, Appl
	15	34.6	3.1	8996	15	US-10-239-676-212	Sequence 212, App
	16	34.4	3.0	414	15	US-10-184-644-314	Sequence 314, App
	17	34.4	3.0	414	15	US-10-184-634-314	Sequence 314, App
	18	34.4	3.0	858	15	US-10-156-761-6230	Sequence 6230, Ap
c	19	34.4	3.0	1506	15	US-10-156-761-5159	Sequence 5159, Ap
	20	34.4	3.0	2617	15	US-10-027-632-262422	Sequence 262422,
	21	34.4	3.0	5234	15	US-10-027-632-262421	Sequence 262421,
	22	33.8	3.0	14649	15	US-10-239-676-122	Sequence 122, App
c	23	33.6	3.0	333	11	US-09-960-352-12655	Sequence 12655, A
c	24	33.4	3.0	365	10	US-09-864-761-27103	Sequence 27103, A
c	25	33.4	3.0	693	15	US-10-156-761-1183	Sequence 1183, Ap
c	26	33.4	3.0	852	15	US-10-267-255-36	Sequence 36, Appl
c	27	33.4	3.0	1539	15	US-10-156-761-75	Sequence 75, Appl
c	28	33.4	3.0	5581	15	US-10-087-993-33	Sequence 33, Appl
	29	33.4	3.0	53500	15	US-10-267-255-76	Sequence 76, Appl
c	30	33.4	3.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
c	31	33.2	2.9	1155	15	US-10-156-761-1636	Sequence 1636, Ap
c	32	32.8	2.9	424	11	US-09-867-701-3179	Sequence 3179, Ap
c	33	32.8	2.9	1049	14	US-10-146-731-358	Sequence 358, App
c	34	32.8	2.9	1049	15	US-10-123-155-358	Sequence 358, App
c	35	32.8	2.9	1533	15	US-10-156-761-779	Sequence 779, App
c	36	32.8	2.9	1805	10	US-09-823-114-18	Sequence 18, Appl
c	37	32.8	2.9	1805	15	US-10-290-748-18	Sequence 18, Appl
c	38	32.8	2.9	1829	12	US-09-905-186A-7	Sequence 7, Appli
c	39	32.8	2.9	1829	12	US-09-905-186A-8	Sequence 8, Appli
c	40	32.8	2.9	1829	12	US-09-905-186A-9	Sequence 9, Appli
c	41	32.8	2.9	1829	12	US-09-905-186A-10	Sequence 10, Appl
c	42	32.8	2.9	1829	12	US-09-905-186A-11	Sequence 11, Appl
c	43	32.8	2.9	2534	15	US-10-087-345A-22	Sequence 22, Appl
c	44	32.8	2.9	2534	15	US-10-225-567A-208	Sequence 208, App
c	45	32.8	2.9	2602	12	US-09-905-186A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-941-945A-1
; Sequence 1, Application US/09941945A
; Patent No. US20020111468A1
; GENERAL INFORMATION:
; APPLICANT: BATHE, Brigitte, et al.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES CODING FOR THE sigD GENE
; FILE REFERENCE: 032301 WD 190

OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 18:13:17 ; Search time 1896 Seconds
                                           (without alignments)
                                           9643.832 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1:   em_estba:*
                 2:   em_esthum:*
                 3:   em_estin:*
                 4:   em_estmu:*
                 5:   em_estov:*
                 6:   em_estpl:*
                 7:   em_estro:*
                 8:   em_htc:*
                 9:   gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: gb_gss:*
                 18: em_gss_hum:*
                 19: em_gss_inv:*
                 20: em_gss_pln:*
                 21: em_gss_vrt:*
                 22: em_gss_fun:*
                 23: em_gss_mam:*
                 24: em_gss_mus:*
                 25: em_gss_other:*
                 26: em_gss_pro:*
                 27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	45.2	4.0	1207	17	CNS015ZN	AL106109 Drosophil
c	2	39	3.5	1101	17	CNS00LO0	AL068607 Drosophil
c	3	39	3.5	1101	17	CNS00ZB7	AL097453 Drosophil
	4	38.6	3.4	1101	17	CNS00LT2	AL078714 Drosophil
	5	37.6	3.3	2072	11	AK016917	AK016917 Mus muscu
c	6	37.2	3.3	435	14	W96254	W96254 ze42b01.r1
c	7	37.2	3.3	444	9	AA018279	AA018279 ze53h06.r
c	8	37.2	3.3	460	9	AA018267	AA018267 ze53g07.r
c	9	37.2	3.3	464	9	AA054016	AA054016 zf48h07.r
c	10	37.2	3.3	493	9	AA013384	AA013384 ze28b12.r
c	11	37.2	3.3	505	14	H86191	H86191 ys94g06.r1
	12	37.2	3.3	807	12	BG321006	BG321006 Zm04_03e1
	13	37.2	3.3	887	13	BI096866	BI096866 SCUMtig11
c	14	37	3.3	389	14	H84094	H84094 ys94f11.r1
c	15	37	3.3	400	14	H84088	H84088 ys94e12.r1
c	16	37	3.3	427	9	AA056119	AA056119 zf55g07.r
	17	36.8	3.3	1101	17	CNS00FCQ	AL070525 Drosophil
c	18	36.6	3.2	421	17	AQ234900	AQ234900 HS_2054_A
c	19	36.6	3.2	475	12	BF412036	BF412036 UI-R-BT1-
c	20	36.6	3.2	704	17	AG171291	AG171291 Pan trogl
	21	36.6	3.2	884	17	CNS006U0	AL065923 Drosophil
	22	36.4	3.2	289	10	AW372518	AW372518 PM3-BT034
c	23	36.4	3.2	541	17	AQ611746	AQ611746 HS_5087_B
c	24	36.4	3.2	565	17	B68684	B68684 CIT-HSP-205
c	25	36.2	3.2	706	13	BM338529	BM338529 MEST228-C
	26	36.2	3.2	797	13	BI829416	BI829416 603080434
	27	36	3.2	1101	17	CNS0100X	AL098379 Drosophil
	28	35.8	3.2	482	17	P752L	AL354014 Leishmani
	29	35.8	3.2	498	17	P332R	AL160657 Leishmani
c	30	35.8	3.2	602	14	BQ200778	BQ200778 UI-R-EB1-
c	31	35.8	3.2	939	17	CNS00CNG	AL059400 Drosophil
	32	35.6	3.2	240	10	BB012808	BB012808 BB012808
c	33	35.6	3.2	895	12	BF166253	BF166253 601777016
	34	35.4	3.1	454	10	AV619431	AV619431 AV619431
c	35	35.4	3.1	506	10	AW308983	AW308983 sf92f04.y
	36	35.4	3.1	591	14	W44028	W44028 mc72g12.r1
	37	35.4	3.1	692	17	BH453605	BH453605 BOHJS75TF
c	38	35.2	3.1	412	17	BH757495	BH757495 SALK_0563
	39	35.2	3.1	543	13	BM330956	BM330956 PIC1_67_F
	40	35.2	3.1	555	13	BM330963	BM330963 PIC1_67_G
	41	35.2	3.1	579	13	BM331661	BM331661 PIC1_59_D
	42	35.2	3.1	582	13	BM318188	BM318188 PI1_79_E0
c	43	35.2	3.1	584	12	BF042140	BF042140 BP250023A
c	44	35.2	3.1	594	12	BF042242	BF042242 BP250021B
	45	35.2	3.1	597	10	BE598653	BE598653 PI1_84_A0

ALIGNMENTS

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 31, 2003, 18:29:46 ; Search time 71 Seconds
                                           (without alignments)
                                           4876.592 Million cell updates/sec

Title: US-09-941-945A-1
Perfect score: 1129
Sequence: 1 catatgcaggcgaactcctg..........ccagtggaatccacttcgga 1129

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                   SUMMARIES
                          %
Result   Query
     No.   Score   Match Length DB   ID   Description
----
       1   133.4   11.8   874   4   US-09-082-920-1   Sequence 1, Appli
  c   2   133.4   11.8 4403765   4   US-09-103-840A-2   Sequence 2, Appli
  c   3   133.4   11.8 4411529   4   US-09-103-840A-1   Sequence 1, Appli
  c   4   34.8   3.1   771   4   US-09-221-017B-667   Sequence 667, App
  c   5   34.4   3.0   1401   2   US-08-812-412-1   Sequence 1, Appli
  c   6   34.4   3.0   1401   4   US-09-180-271-4   Sequence 4, Appli
  c   7   34.2   3.0   7218   1   US-08-232-463-14   Sequence 14, Appl
       8   33.8   3.0   1420   3   US-09-362-506-1   Sequence 1, Appli
  c   9   32.8   2.9   1805   4   US-08-405-271A-18   Sequence 18, Appl
      10   32.6   2.9   2588   2   US-08-796-414B-6   Sequence 6, Appli
  c   11   32.6   2.9   30001   1   US-08-125-468-1   Sequence 1, Appli